Kaufman

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/099,898*

DATE: 11/04/98
TIME: 19:06:26

INPUT SET: S29635.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

ENTERED

```
 1                               SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5       (i) APPLICANT: Franz-Bacon, Karin
 6                     Gorman, Daniel M.
 7                     McClanahan, Terrill K.
 8
 9      (ii) TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
10
11     (iii) NUMBER OF SEQUENCES: 4
12
13      (iv) CORRESPONDENCE ADDRESS:
14           (A) ADDRESSEE: DNAX Research Institute
15           (B) STREET: 901 California Avenue
16           (C) CITY: Palo Alto
17           (D) STATE: California
18           (E) COUNTRY: USA
19           (F) ZIP: 94304-1104
20
21       (v) COMPUTER READABLE FORM:
22           (A) MEDIUM TYPE: Floppy disk
23           (B) COMPUTER: IBM PC compatible
24           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27      (vi) CURRENT APPLICATION DATA:
28           (A) APPLICATION NUMBER: US not yet assigned
29           (B) FILING DATE: 18-JUN-1998
30           (C) CLASSIFICATION:
31
32     (vii) PRIOR APPLICATION DATA:
33           (A) APPLICATION NUMBER: US 60/050,156
34           (B) FILING DATE: 17-JUN-1997
35
36    (viii) ATTORNEY/AGENT INFORMATION:
37           (A) NAME: Ching, Edwin P.
38           (B) REGISTRATION NUMBER: 34,090
39           (C) REFERENCE/DOCKET NUMBER: DX0744K
40
41      (ix) TELECOMMUNICATION INFORMATION:
42           (A) TELEPHONE: 650-852-9196
43           (B) TELEFAX: 650-496-1200
44
45
46   (2) INFORMATION FOR SEQ ID NO:1:
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INPUT SET: S29635.raw

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47
48          (i) SEQUENCE CHARACTERISTICS:
49               (A) LENGTH: 453 base pairs
50               (B) TYPE: nucleic acid
51               (C) STRANDEDNESS: single
52               (D) TOPOLOGY: linear
53
54         (ii) MOLECULE TYPE: cDNA
55
56
57         (ix) FEATURE:
58               (A) NAME/KEY: CDS
59               (B) LOCATION: 47..370
60
61         (ix) FEATURE:
62               (A) NAME/KEY: mat_peptide
63               (B) LOCATION: 101..370
64
65
66         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67
68  GTGTGCCGGA TTTGGTTAGC TGAGCCCACC GAGAGGCGCC TGCAGG ATG AAA GCT      55
69                                                        Met Lys Ala
70                                                        -18
71
72  CTC TGT CTC CTC CTC CTC CCT GTC CTG GGG CTG TTG GTG TCT AGC AAG    103
73  Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val Ser Ser Lys
74  -15                 -10                 -5                    1
75
76  ACC CTG TGC TCC ATG GAA GAA GCC ATC AAT GAG AGG ATC CAG GAG GTC    151
77  Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile Gln Glu Val
78               5                  10                 15
79
80  GCC GGC TCC CTA ATA TTT AGG GCA ATA AGC AGC ATT GGC CTG GAG TGC    199
81  Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly Leu Glu Cys
82           20                  25                  30
83
84  CAG AGC GTC ACC TCC AGG GGG GAC CTG GCT ACT TGC CCC CGA GGC TTC    247
85  Gln Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro Arg Gly Phe
86       35                  40                  45
87
88  GCC GTC ACC GGC TGC ACT TGT GGC TCC GCC TGT GGC TCG TGG GAT GTG    295
89  Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser Trp Asp Val
90   50                  55                  60                  65
91
92  CGC GCC GAG ACC ACA TGT CAC TGC CAG TGC GCG GGC ATG GAC TGG ACC    343
93  Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met Asp Trp Thr
94               70                  75                  80
95
96  GGA GCG CGC TGC TGT CGT GTG CAG CCC TGAGGTCGCG CGCAGCGCGT          390
97  Gly Ala Arg Cys Cys Arg Val Gln Pro
98           85                  90
99
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100   GCACAGCGCG GGCGGAGGCG GCTCCAGGTC CGGAGGGGTT GCGGGGGAGC TGGAAATAAA      450
101
102   CCT                                                                    453
103
104
105   (2) INFORMATION FOR SEQ ID NO:2:
106
107         (i) SEQUENCE CHARACTERISTICS:
108               (A) LENGTH: 108 amino acids
109               (B) TYPE: amino acid
110               (D) TOPOLOGY: linear
111
112         (ii) MOLECULE TYPE: protein
113
114         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
115
116   Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val
117   -18         -15                 -10                 -5
118
119   Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile
120            1               5                   10
121
122   Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly
123    15                 20                  25                  30
124
125   Leu Glu Cys Gln Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro
126                 35                  40                  45
127
128   Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser
129             50                  55                  60
130
131   Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met
132            65                  70                  75
133
134   Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
135        80                  85                  90
136
137   (2) INFORMATION FOR SEQ ID NO:3:
138
139         (i) SEQUENCE CHARACTERISTICS:
140               (A) LENGTH: 24 base pairs
141               (B) TYPE: nucleic acid
142               (C) STRANDEDNESS: single
143               (D) TOPOLOGY: linear
144
145         (ii) MOLECULE TYPE: cDNA
146
147
148
149
150         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
151
152   TGTGGCTHYG SCTGTGGMTC KTGG                                               24
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153
154    (2) INFORMATION FOR SEQ ID NO:4:
155
156        (i) SEQUENCE CHARACTERISTICS:
157            (A) LENGTH: 23 base pairs
158            (B) TYPE: nucleic acid
159            (C) STRANDEDNESS: single
160            (D) TOPOLOGY: linear
161
162    (ii) MOLECULE TYPE: cDNA
163
164
165
166
167        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
168
169    CAGCAGCGSG CWSHKGTCCA GTC                                        23
170
171
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